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RAW SEQUENCE LISTING

DATE: 11/28/2001

PATENT APPLICATION: US/09/922,683

TIME: 10:38:37

Input Set : N:\Crf3\RULE60\09922683.txt

Output Set: N:\CRF3\11282001\I922683.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: DECKER, Heinrich

8 (ii) TITLE OF INVENTION: ISOLATION OF THE BIOSYNTHESIS GENES FOR

9 PSEUDO-OLIGOSACCHARIDES FROM STREPTOMYCES GLAUDESCENS

10 GLA. O AND THEIR USE

12 (iii) NUMBER OF SEQUENCES: 13

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: FOLEY & LARDNER

16 (B) STREET: 3000 K Street, N.W.

17 (C) CITY: Washington

18 (D) STATE: D.C.

19 (E) COUNTRY: U.S.A.

20 (F) ZIP: 20007-5109

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk

24 (B) COMPUTER: IBM PC compatible

25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/09/922,683

C--> 30 (B) FILING DATE: 07-Aug-2001

31 (C) CLASSIFICATION:

37 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: 09/194,905

35 (B) FILING DATE: 1999-12-01

38 (A) APPLICATION NUMBER: DE 19622783.6

39 (B) FILING DATE: 07-JUN-1996

41 (viii) ATTORNEY/AGENT INFORMATION:

42 (A) NAME: Granados, Patricia D.

43 (B) REGISTRATION NUMBER: 33,683

44 (C) REFERENCE/DOCKET NUMBER: 026083/0193

46 (ix) TELECOMMUNICATION INFORMATION:

47 (A) TELEPHONE: (202) 672-5300

48 (B) TELEFAX: (202) 672-5399

51 (2) INFORMATION FOR SEQ ID NO: 1:

53 (i) SEQUENCE CHARACTERISTICS:

54 (A) LENGTH: 22 base pairs

55 (B) TYPE: nucleic acid

56 (C) STRANDEDNESS: single

57 (D) TOPOLOGY: linear

59 (ii) MOLECULE TYPE: other nucleic acid

60 (A) DESCRIPTION: /desc = "Primer"

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

67 CSGGSGSSGC SGGSTTCATS GG

69 (2) INFORMATION FOR SEQ ID NO: 2:

71 (i) SEQUENCE CHARACTERISTICS:

ENTERED

22

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72      (A) LENGTH: 24 base pairs
73      (B) TYPE: nucleic acid
74      (C) STRANDEDNESS: single
75      (D) TOPOLOGY: linear
77      (ii) MOLECULE TYPE: other nucleic acid
78      (A) DESCRIPTION: /desc = "Primer"
83      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
85 GGGWVCTGGY VSGGSCCGTA GTTG                                     24
87 (2) INFORMATION FOR SEQ ID NO: 3:
89      (i) SEQUENCE CHARACTERISTICS:
90          (A) LENGTH: 546 base pairs
91          (B) TYPE: nucleic acid
92          (C) STRANDEDNESS: single
93          (D) TOPOLOGY: linear
95      (ii) MOLECULE TYPE: DNA (genomic)
100     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
102 CCCGGGCGGG GCGGGGTTCA TCGGCTCCGC CTACGTCCGC CGGCTCCTGT CGCCCGGGGC      60
104 CCCCGGCGGC GTCGCGGTGA CCGTCTCGA CAAACTCACC TACGCCGGA GCCTCGCCCG      120
106 CCTGCACGCG GTGCGTGACC ATCCCGCCT CACCTTCGTC CAGGGCGACG TGTGCGACAC      180
108 CGCGCTCGTC GACACGCTGG CCGCGCGGCA CGACGACATC GTGCACTTCG CGGCCGAGTC      240
110 GCACGTCGAC CGTCCATCA CCGACAGCGG TGCCTTCACC CGCACCAACG TGCTGGGCAC      300
112 CCAGGTCCTG CTCGACGCCG CGTCCGCCA CGGTGTGCGC ACCCTCGTGC ACGTCTCCAC      360
114 CGACGAGGTG TACGGCTCCC TCCCGCACGG GGCCGCCGCG GAGAGCGACC CCCTGCTCCC      420
116 GACCTCGCCG TACGCGGCGT CGAAGGCGGC CTCGGACCTC ATGGCGCTCG CCCACCACCG      480
118 CACCACGGC CTGGACGTCC GGGTGACCCG CTGTTCGAAC AACTACGGCC CGCACCAGTT      540
120 CCCGGG                                     546
122 (2) INFORMATION FOR SEQ ID NO: 4:
124     (i) SEQUENCE CHARACTERISTICS:
125         (A) LENGTH: 541 base pairs
126         (B) TYPE: nucleic acid
127         (C) STRANDEDNESS: single
128         (D) TOPOLOGY: linear
130     (ii) MOLECULE TYPE: DNA (genomic)
135     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
137 CCCCGGGTGC TGGTAGGGGC CGTAGTTGTT GGAGCAGCGG GTGATGCGCA CGTCCAGGCC      60
139 GTGGCTGACG TGCATGGCCA GCGCGAGCAG GTCGCCCCGAC GCCTTGAGAG TGGCATAGGG      120
141 GCTGTTGGGG CGCAGCGGCT CGTCTCCCGT CCACGACCCC GTCTCCAGCG AGCCGTAGAC      180
143 CTCGTCGGTG GACACCTGCA CGAAGGGGGC CACGCCGTGC CGCAGGGCCG CGTCGAGGAG      240
145 TGTCTGCGTG CCGCCGGCGT TGGTCCGCAC GAACGCGGCG GCATCGAGCA GCGAGCGGTC      300
147 CACGTGCGAC TCGGCGGCGA GGTGCACGAC CTGGTCTCTGG CCGGCCATGA CCCGGTCGAC      360
149 CAGGTCCGCG TCGCAGATGT CGCCGTGGAC GAAGCGCAGC CGGGGGTGGT CGCGGACCGG      420
151 GTCGAGGTTG GCGAGGTTGC CGGCGTAGCT CAGGGCGTCG AGCACGGTGA CGACGGCGTC      480
153 GGGCGGCCCG TCCGACCGA GGAGGGTGCG GACGTAGTGC GAGCCCATGA ACCCGCCCGC      540
155 C                                     541
157 (2) INFORMATION FOR SEQ ID NO: 5:
159     (i) SEQUENCE CHARACTERISTICS:
160         (A) LENGTH: 180 amino acids
161         (B) TYPE: amino acid
162         (C) STRANDEDNESS:

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163      (D) TOPOLOGY: linear
165      (ii) MOLECULE TYPE: protein
170      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
172      Ala Ala Gly Phe Met Gly Ser His Tyr Val Arg Thr Leu Leu Gly Pro
173      1          5          10          15
175      Asp Gly Pro Pro Asp Ala Val Val Thr Val Leu Asp Ala Leu Ser Tyr
176      20          25          30
178      Ala Gly Asn Leu Ala Asn Leu Asp Pro Val Arg Asp His Pro Arg Leu
179      35          40          45
181      Arg Phe Val His Gly Asp Ile Cys Asp Ala Asp Leu Val Asp Arg Val
182      50          55          60
184      Met Ala Gly Gln Asp Gln Val Val His Leu Ala Ala Glu Ser His Val
185      65          70          75          80
187      Asp Arg Ser Leu Leu Asp Ala Ala Ala Phe Val Arg Thr Asn Ala Gly
188      85          90          95
190      Gly Thr Gln Thr Leu Leu Asp Ala Ala Leu Arg His Gly Val Ala Pro
191      100         105         110
193      Phe Val Gln Val Ser Thr Asp Glu Val Tyr Gly Ser Leu Glu Thr Gly
194      115         120         125
196      Ser Trp Thr Glu Asp Glu Pro Leu Arg Pro Asn Ser Pro Tyr Ala Thr
197      130         135         140
199      Ser Lys Ala Ser Gly Asp Leu Leu Ala Leu Ala Met His Val Ser His
200      145         150         155         160
202      Gly Leu Asp Val Arg Ile Thr Arg Cys Ser Asn Asn Tyr Gly Pro Tyr
203      165         170         175
205      Gln His Pro Gly
206      180
208 (2) INFORMATION FOR SEQ ID NO: 6:
210      (i) SEQUENCE CHARACTERISTICS:
211          (A) LENGTH: 181 amino acids
212          (B) TYPE: amino acid
213          (C) STRANDEDNESS:
214          (D) TOPOLOGY: linear
216      (ii) MOLECULE TYPE: protein
221      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
223      Pro Gly Gly Ala Gly Phe Ile Gly Ser Ala Tyr Val Arg Arg Leu Leu
224      1          5          10          15
226      Ser Pro Gly Ala Pro Gly Gly Val Ala Val Thr Val Leu Asp Lys Leu
227      20          25          30
229      Thr Tyr Ala Gly Ser Leu Ala Arg Leu His Ala Val Arg Asp His Pro
230      35          40          45
232      Gly Leu Thr Phe Val Gln Gly Asp Val Cys Asp Thr Ala Leu Val Asp
233      50          55          60
235      Thr Leu Ala Ala Arg His Asp Asp Ile Val His Phe Ala Ala Glu Ser
236      65          70          75          80
238      His Val Asp Arg Ser Ile Thr Asp Ser Gly Ala Phe Thr Arg Thr Asn
239      85          90          95
241      Val Leu Gly Thr Gln Val Leu Leu Asp Ala Ala Leu Arg His Gly Val
242      100         105         110

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244 Arg Thr Leu Val His Val Ser Thr Asp Glu Val Tyr Gly Ser Leu Pro
 245 115 120 125
 247 His Gly Ala Ala Ala Glu Ser Asp Pro Leu Leu Pro Thr Ser Pro Tyr
 248 130 135 140
 250 Ala Ala Ser Lys Ala Ala Ser Asp Leu Met Ala Leu Ala His His Arg
 251 145 150 155 160
 253 Thr His Gly Leu Asp Val Arg Val Thr Arg Cys Ser Asn Asn Tyr Gly
 254 165 170 175
 256 Pro His Gln Phe Pro
 257 180

259 (2) INFORMATION FOR SEQ ID NO: 7:

261 (i) SEQUENCE CHARACTERISTICS:

262 (A) LENGTH: 6854 base pairs

263 (B) TYPE: nucleic acid

264 (C) STRANDEDNESS: single

265 (D) TOPOLOGY: linear

267 (ii) MOLECULE TYPE: DNA (genomic)

272 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

274 CTGCAGGGTT CCCTGGTGCA CGACCCGCCC CTGGTCGACG ACCAGGGGCGC TGTCGCAGAT 60
 276 CGCGGCGATG TCGGCGATGT CGTGGCTGGT GAGCACCACG GTGGTGCCCA GTTCCCGGTG 120
 278 GGCGCGGTTG ACCAGCCGGC GCACCGCGTC CTTCAGCACC ATGTCGAGGC CGATCGTGGG 180
 280 CTCGTCCAG AACAGCACGG CCGGGTCGTG CAGCAGGCTC GCCGCGATCT CGGCGCGCAT 240
 282 GCGCTGTCCG AGGCTGAGCT GCCGCACGGG GGTGGACCCC AGCGCGTCGA TGTCGAGGAG 300
 284 GTCCCGGAAC AGGGCGAGGT TGCGCCGGTA GACCGGTCCG GGGATGTCGT AGATGCGGCG 360
 286 CAGGATGCGG AAGGAGTCGG GTACCGACAG GTCCCACCAG AGCTGGCTGC GCTGGCCGAA 420
 288 GACGACGCCG ATCGTGCGGG CGTTGCGCTG CCGGTGCCGG TAGGGCTCCA GCGCGCGAC 480
 290 CGTGACGCGG CCGGAGGTGG GGGTCATGAT GCCGGTCAGC ATCTTGATCG TGGTCGACTT 540
 292 GCCGGCTCCG TTGGCGCCGA TGTAGGCGGT CTTCGTGCCG GCCGGTATCT CGAAGGAGAC 600
 294 GTCGTCGACG GCGCGCACGA CGCGGTACCG GCGGGTCAGG AGGGTGGAGA GGCTGCCGAG 660
 296 CAGGCCGGGC TCGCGTTCGG CCAGCCGGAA CTCCTTGACG AGGTGTTTCG CCACGATCAC 720
 298 GCGATCACCC GCTCGACGGC CGTCTCCAGC AGGCGCAGGC CCTCGTCGAG CAGCGCCTCG 780
 300 TCGAGGGTGA ACGGCGGTGC CAGCCGCAAG ATGTGGCCGC CCAGGGAGGT GCGCAGCCCC 840
 302 AGGTCGAGGG CGGTGGTGTA GACGGCCCCG GCGGTCTCGG GGGCGGGTGC CCGGCCGACG 900
 304 GCGTCGGTGA CGAACTCCAG GCCCCACAGC AGTCCGAGGC CGCGTACCTG GCCGAGCTGG 960
 306 GGGAAGCGGG ACTCCAGGGC GCGCAGCCGC TCCTGGATGA GCTCGCCGAG GACGCGCACG 1020
 308 CGGTCGATCA GCCGGTCGCG CTCGACGACC TCCAGCGTGG CGCGGGCGGC GGCGATCCCC 1080
 310 AGTGGGTTGC TCGCGTACGT CGAGGCGTAC GCGCGGGGGT GGCGGCCTCC GGCCTGCGCA 1140
 312 GCTTCCGCGC GTCCGGCCAG CACGGCGAAG GGGAATCCGC TCGCGGTGCC CTTGGACAGC 1200
 314 ATCGCCAGGT CCGGCTCGAT GCCGAACAGT TCGCTGGCGA GGAAGGCGCC GGTGCGCCCC 1260
 316 CCGCCGGTGA GGACCTCGTC GGCGACGAGC AGCAGCCGC CGTCCCGGCA GGCGCCGGCG 1320
 318 ATCCGCTCCC AGTAGCCGGG GGGCGGCACG ATGACGCCTG CCGCGCCGAG GACGGGTTTC 1380
 320 AAGACCAGGG CCGAGACGTT GGGCTTCTCC GCGATGTGCC GGCGCACGAG GGTGCGGCAC 1440
 322 CGCACGTCGC ACGAGGGGTA CTCCAGGCCC AGGGGACAGC GGTAGCCAGT AGGGGCTGTA 1500
 324 GCCAGCACGC TGTGCGCGCT GAAGGCCTGG TGGCCGATGT CCCAGTGGAC CAGCATCCGG 1560
 326 GCGCCCATGG TCTTGCCGTG GAAGCCGTGG CGCAGGGCGC AGATCCGGTT GCGGCCCGGC 1620
 328 GCGGCGGTGC CCTGGACGAC CCGCAGGGCG GCCTCGACCA CCTCCGCGCC GGTGGAGAAG 1680
 330 AAGGCGTAGG TGTCGAGCTC TTCCGCCACC ACCCTGGCCA GCAGTTCCAG CAGGCCGGCG 1740
 332 CGGTCCGGCG TGGCGGTGTC GTGGACGTTT CACAGGCGGC GGGCCTGGGT GGTGAGTGCC 1800
 334 TCGACGACCT CCGGGTGCCC GTGGCCAGT GACTGGGTGA GGGTCCCGGC CGCGAAGTCG 1860

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336	AGGTACTGGT	TGCCGTCCAG	GTCGGTCAGA	ACGGGACCGC	GTCCCTCGGC	GAAGACCCGG	1920
338	CGTCCGTGGA	CGGCTTCCTC	GGAGGCGCCC	GGCGCCAGGT	GGCGGGCCTC	CCGTGCCAGG	1980
340	TGCTGTGTCT	GCCGTAAGCC	TGTCATCGCT	GCCTCTGCTC	GTCGGACCGG	CTGACGCGAT	2040
342	CGCCGGCGAA	CTGCGTTGTG	GCGCACCACG	GTTGGGGCGG	CTCGGCGCTG	AGTCAAACAC	2100
344	TTGAACACAC	ACCCTGCAA	GAGTTTGCGG	GTTGTTTCAG	AAAGTTGTTG	CGAGCGGCCC	2160
346	CGGCACTCTG	GTTGAGTCGA	CGTGCTTACG	GCGCCACCAC	GCCTCACGTT	CGAGGAGGGA	2220
348	CCTGTGAGAA	CAAGCCCGCA	GACCGACCCG	CTCCCGCGGA	GGCCGAGGTG	AAGGCCCTGG	2280
350	TCCTGGCAGG	TGGAACCGGC	AGCAGACTGA	GGCCGTTTAC	CCACACCGCC	GCCAAGCAGC	2340
352	TGCTCCCAT	CGCCAACAAG	CCCGTGCTCT	TCTACGCGCT	GGAGTCCCTC	GCCGCGGCGG	2400
354	GTGTCCGGA	GGCCGGCGTC	GTCGTGGGCG	CGTACGGCCG	GGAGATCCGC	GAACTCACCG	2460
356	GCGACGGCAC	CGCGTTCGGG	TTACGCATCA	CCTACCTCCA	CCAGCCCGCG	CCGCTCGGTC	2520
358	TCGCGCACGC	GGTGCGCATC	GCCC CGGGCT	TCCTGGGCGA	CGACGACTTC	CTGCTGTACC	2580
360	TGGGGGACAA	CTACCTGCCC	CAGGGCGTCA	CCGACTTCGC	CCGCCAATCG	GCCGCCGATC	2640
362	CCGCGGCGGC	CCGGCTGCTG	CTCACCCCGG	TCGCGGACCC	GTCCGCCTTC	GGCGTCGCGG	2700
364	AGGTCGACGC	GGACGGGAAC	GTGCTGCGCT	TGGAGGAGAA	ACCCGACGTC	CCGCGCAGCT	2760
366	CGCTCGCGCT	CATCGGCGTG	TACGCCTTCA	CCCCGCCCGT	CCACGAGGCG	GTACGGGCCA	2820
368	TCACCCCTC	CGCCCCGCGC	GAGCTGGAGA	TCACCCACGC	CGTGCACTGG	ATGATCGACC	2880
370	GGGGCCTGCG	CGTACGGGCC	GAGACCACCA	CCCCGCCCTG	GCGCGACACC	GGCAGCGCGG	2940
372	AGGACATGCT	GGAGGTCAAC	CGTCACGTCC	TGGACGGAAT	GGAGGGCCGC	ATCGAGGGGA	3000
374	AGGTCGACGC	GCACAGCACG	CTGGTCGGCC	GGGTCCGGGT	GGCCGAAGGC	GCGATCGTGC	3060
376	GGGGGTACAA	CGTGGTGGGC	CCGGTGGTGA	TCGGCGCGGG	TGCCGTCTGC	AGCAACTCCA	3120
378	GTGTGCGCCC	GTACACCTCC	ATCGGGGAGG	ACTGCCGGGT	CGAGGACAGC	GCCATCGAGT	3180
380	ACTCCGTCCT	GCTGCGCGGC	GCCCAGGTCG	AGGGGGCGTC	CCGCATCGAG	GCGTCCCTCA	3240
382	TCGGCCGCGG	CGCCGTCTGC	GGCCCGGCCC	CCCGTCTCCC	GCAGGCTCAC	CGACTGGTGA	3300
384	TCGGCGACCA	CAGCAAGGTG	TATCTACCCC	CATGACCACG	ACCATCCTCG	TCACCGGCGG	3360
386	AGCGGGCTTC	ATTCGCTCCG	CCTACGTCCG	CCGGCTCCTG	TCGCCCCGGG	CCCCCGGCGG	3420
388	CGTCGCGGTG	ACCGTCCCTG	ACAAACTCAC	CTACGCCGGC	AGCCTCGCCC	GCCTGCACGC	3480
390	GGTGCGTGAC	CATCCCGGCC	TCACCTTCGT	CCAGGGCGAC	GTGTGCGACA	CCGCGCTCGT	3540
392	CGACACGCTG	GCCGCGCGGC	ACGACGACAT	CGTGCACTTC	GCGGCCGAGT	CGCACGTCTGA	3600
394	CCGCTCCATC	ACCACAGCGG	GTGCCTTCAC	CCGCACCAAC	GTGCTGGGCA	CCCAGGTCTT	3660
396	GCTCGACGCC	GCGCTCCGCC	ACGGTGTGCG	CACCTTCGTG	CACGTCTCCA	CCGACGAGGT	3720
398	GTACGGCTCC	CTCCCGCACG	GGGCCGCCGC	GGAGAGCGAC	CCCCTGCTTC	CGACCTCGCC	3780
400	GTACGCGGCG	TCGAAGGCGG	CCTCGGACCT	CATGGCGCTC	GCCCACCACC	GCACCCACGG	3840
402	CCTGGACGTC	CGGGTGACCC	GCTGTTGAA	CAACTTCGGC	CCCCACCAGC	ATCCCCGAGAA	3900
404	GCTCATACCG	CGCTTCCTGA	CCAGCCTCCT	GTCCGGCGGC	ACCGTTCCCC	TCTACGGCGA	3960
406	CGGGCGGCAC	GTGCGCGACT	GGCTGCACGT	CGACGACCAC	GTCAGGGCCG	TCGAACCTCGT	4020
408	CCGCGTGTCT	GGCCGGCCCG	GAGAGATCTA	CAACATCGGG	GGCGGCACCT	CGCTGCCCAA	4080
410	CCTGGAGCTC	ACGCACCGGT	TGCTCGCACT	GTGCGGCGCG	GGCCCGGAGC	GCATCGTCCA	4140
412	CGTCGAGAAC	CGCAAGGGGC	ACGACCGGCG	CTACGCGGTC	GACCACAGCA	AGATCACCGC	4200
414	GGAACCTCGT	TACCGGCCGC	GCACCGACTT	CGCGACCGCG	CTGGCCGACA	CCGCGAAGTG	4260
416	GTACGAGCGG	CACGAGGACT	GGTGGCGTCC	CCTGCTCGCC	GCGACATGAC	GTGGGGCCGG	4320
418	ACCGCAACCA	CCGGCCCCCG	CCGGCACACC	GCCGCCCGCG	GCCGGTGGCC	GGCCGGTCAG	4380
420	CGTCCGTGAG	CCGGGCGCCG	GCCGCCCGCG	GGGCCGGCGG	CGGTGGACCC	CCGACCACC	4440
422	AGTTCCGGCA	TGAAGACGAA	TTGGTTCGCG	GGCGGCGGCG	TTCCGCTCAT	CTCCTCCAGC	4500
424	AGTGCGTCCA	CGGCGACCTG	CCCCATCGCC	TTGACGGGCT	GTCTGATGGT	GGTCAGGGGA	4560
426	GGGTGCGTGA	AGGCCATGAG	CGGCGAGTCG	TCGAAGCCGA	CCACCGAGAT	GTCACCGGGA	4620
428	ACCGTGAGAC	CCCGCCGGCG	CGCGGCCCGC	ACGGCGCCCA	CGCCCATCAT	GTCGCTGGCG	4680
430	CACATGACGG	CGGTGCAGCC	CAGGTGCGATC	AGCGCGGACG	CGGCGGCGCTG	GCCCCCTTCC	4740
432	AGGGAGAACA	GCGAGTGCTG	CACGAGCTCC	TCGGACTCCC	GCGCCGACAC	TCCCAGGTGC	4800

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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]